

STATISTICAL EXAMINATION OF YIELD AND QUALITY COMPONENTS IN WHEAT (*T.aestivum* L.)

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ABSTRACT. The aim of this study was to determine certain characters, having significant effect in seed yield and protein content by statistical analyze methods, conditional formatting, correlation and path, multiple linear stepwise regression, factor, biplot, decision tree and phyton regression analyzes in bread wheat. This study was carried out under arid conditions in the experimental field of the Faculty of Agriculture of ESOGU during the cultivation period of 2019-2020 and 2020-2021. In the study, seed yield, heading day, plant height, seed number and weight/spike, spike length, SPAD, chlorophyll a and b, thousand seed weight, test weight, protein content, micro sedimentation were examined. The two-year averages of the results of the examined elements were taken into account and statistical analyzes were made on these results. As statistical analyzes; conditional formatting, correlation and path, multiple linear stepwise regression, factor, biplot, decision tree and phyton regression were used. It was determined that seed number/spike, seed weight/spike, micro sedimentation, SPAD, chlorophyll a and chlorophyll b were were found to be effective parameters on seed yield and protein content.

Keywords: Bread wheat, genotype, yeld and quality components, conditional formatting, correlation and path, multiple linear stepwise regression, factor, biplot, decision tree and phyton regression analyses

INTRODUCTION

Wheat, which is an important species among cereals, occupies an important place in the world's nutrition and ranks first in the world in terms of cultivation and production [1, 2]. Besides, wheat is very important in meeting the food needs of people, with its high adaptability, harvesting, transportation, storage and conversion into product, especially in terms of the nutrients it contains. In addition, products such as flour, bread, pasta, biscuits obtained from wheat are important in human nutrition; Bran and stems are used as a source of carbohydrates in animal nutrition [3, 4, 5]. In order to provide a balanced diet for the growing population in the world, it is necessary to increase the production. For this purpose, it is necessary to use proprietary varieties with high yield, quality, and resistant to biotic and abiotic stresses. In addition, agronomic requirements such as appropriate planting methods, fertilization, irrigation, and weed control are required for high yields [6, 7, 8]. In bread wheat breeding programs; developing high yielding, disease and pest resistant, stabile and adapted, cold and drought resistant, good quality genotypes are needed. With the breeding programs carried out in recent years, high yielding and quality, disease and pest resistant genotypes have been developed and given to use of farmers/producers [8, 9, 10]. It has been stated that chlorophyll measurements at certain periods during plant development contribute to high yield [11, 12, 13]. Again, considering yield components such as the spike number/m², plant height, seed number and weight/spike and using them in breeding programs will provide significant advantages in

development high-yielding genotypes [10, 14, 15]. Genotypes keeping plant height almost same should be selected for high-yielding genotype development for dry conditions [16]. In addition, the effective use of quality components such as test weight, protein content, thousand seed weight and gluten content in breeding programs is very important in the development of high quality genotypes [17, 18].

In the last thirty years, the bread wheat breeding vision has shifted to the development of high yielding and quality genotypes, and protein content, sedimentation, thousand-seed weight and test weight have been revealed as the most important components for high yield and quality [19, 20]. Meanwhile, in recent years, many statistical methods have been used to determine the components affecting yield and quality [21, 22]. For this purpose, statistical methods such as correlation and path, stepwise regression, factor and biplot analysis have been used as effective methods to determine the effective componentss [21, 22, 23]. In this study, the effective components affecting seed yield and protein content were aimed to determine by conditional formatting, correlation and path, multiple linear stepwise regression, factor, biplot, decision tree and phyton regression analyses in bread wheat.

MATERIALS AND METHODS

This study was carried out in the experimental area of the Faculty of Agriculture, ESOGU during the cultivation period of 2019-2020 and 2020-2021 under arid conditions. Some climatic data of the vegetation period of 2019-2020 and 2020-2021 were given in Table 1.

	2019/	2020	2020/	2021	Long Term Me	Long Term Mean (1970-2021)		
Months	Precipitation	Mean Temp.	Precipitation	Mean Temp.	Precipitation	Mean Temp.		
	(IIIII)	(-C)	(IIIII)	(-C)	(IIIII)	(-C)		
October	20,8	15	39,5	17	18	13,2		
November	18,9	10,3	28,2	12,4	27,5	7,3		
December	32,8	3,9	43,6	6	31,5	2,5		
January	39	-3,6	50,4	-0,4	40,5	0,2		
February	28,2	-2,3	41,5	0,9	35,3	1,7		
March	34,7	1,6	34,4	3,7	39,3	5,7		
April	36,8	8,2	19,4	10,3	42,2	11,2		
May	22,7	12,9	19,8	15	51,3	16,1		
June	35,8	16,8	7,5	16,8	35,2	20		
Tot/Mean	269,7	7,0	284,3	9,1	320,8	8,7		

Table 1. Some climatic data in vegetation period of 2019-2020 and 2020-2021.

As seen in Table 1, the total precipitations for the nine months in 2019-2020 and 2020-2021 were 269,7 mm and 284,3 mm, less than the total precipitation for long-term years (320,8 mm). Again, the nine-month average temperature was 7,0°C in 2019-2020 and 9,1°C in 2020-2021. The average temperature for long-term years was 8.7°C. The soil in the study area had a clay-loamy texture and the lime level was moderately high and slightly alkaline. Soil was poor in organic matter. Bread wheat genotypes, Müfitbey, Atay-85, Çetinel-2000, Bayraktar-2000, Alpu-01, Bezostaja-1, Rumeli, Tosunbey, ES-26, Reis, Palandöken-97, Ayyıldız, Altay-2000, Yıldırım, Eser, Demir-2000, Gerek-79, Yunus, Sultan-95, Sönmez-2001, Atay-85, Zencirci, İkizce and Harmankaya-99, were used in the study. The study was set up in a randomized block design with 3 replications. The sowing was made between 1-15 October with a seed drill at 20 cm row spacing (6 m x 1.20 m = 7.6 m², 650 seeds/m²). 0,06 t/ha P2O5 and 0,06 t N/ha fertilizer were applied to bread wheat varieties. All of the phosphorus was given with the planting. Half of the

nitrogen was applied by dividing it into two, with the other half during the sowing period. As weed control, 1600 cc/ha weed control was made with 2,4-D amine weed pesticide against broad-leaved weeds during the early stemming period.

In the experiment, seed yield (t/ha) [24], heading date (days) [25], plant height (cm) [26], seed number and weight(g) [27, 28], of spike number/m² [29], spike length (cm) [30], SPAD [31], chlorophyll a and b [32], thousand seed weight (g) [33], test weight (kg/hl) [34], protein content (%) [35, 36], micro sedimentation (ml) [37], was examined. The averages of two years in components examined were taken into account and statistical analyses were made on these results. As statistical analyse methods; conditional formatting, correlation and path, multiple linear stepwise regression, factor, biplot, decision tree and phyton regression analysis methods were used.

RESULTS AND DISCUSSION

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Inadequate and unbalanced nutrition is one of the most important issues all countries of the world today. For this purpose, the aim of wheat breeding activities in the world; is to develop wheat genotypes, high yielding, high quality, adapted to different environments and years, stabile, resistant to winter, drought, diseases, lodging and meet the demands of consumers, industrialists and producers. [29, 31,34, 35, 36]. In the breeding studies carried out in recent years, main purpose was to apply fast and effective components in selecting and developing promising novel genotypes [27, 28, 25, 36]. For this purpose, different yield and quality components were analysed according to many statistical methods, and the effects of common elements revealed by these methods on yield/quality.

Conditional Formatting Analysis

In recent years, the conditional formatting analysis method has found its place in breeding and has started to be used. In this method, the components discussed were presented in different indicator chart values from the smallest to the largest, and the averages of these components could be evaluated practically and effectively [38, 39]. The yield and quality components examined in our study were evaluated according to the conditional formatting method, and the results were given in Table 2. As seen in Table 2, yield and quality components were evaluated one by one and analysed together. Alpu-01 genotype in seed yield, spike length, chlorophyll a, chlorophyll b and seed weight/spike, Müfitbey genotype in heading date, Bayraktar 2000 genotype in plant height, Ayyıldız genotype in the seed number of/spike, Palandöken-97 genotype in spike number/m², Bejostaja-1 genotype in SPAD gave the highest values. As a means of yield components, Bezostaja-1, Rumeli and Palandöken-97 were determined as the best genotypes (Table 2). Considering the quality components, Rumeli genotype gave highest values in thousand seed weight and protein content.

Micro Sed	15,11	14,28	16,29	12,97	15,29	15,81	16,23	14,23	14,16	14,26	14,3	13,92	14,96	14,98	15,56	15,05	13,89	13,52	13,42	15,14	14,92	15,17	13,51	13,44
Protein C	11.02	11,64	12,91	9,93	11,98	12,75	13	11,03	11,97	10,88	11,91	10,89	11,49	11,59	11,91	11,94	10,39	10,16	10,02	11,98	11,67	11,81	10,31	10,06
Test W	77,13	72,39	72,72	76,63	77,63	78,53	78,91	74,29	74,6	71,88	76,71	73,23	73,43	76,96	78,81	76,13	70,77	68,24	70,41	74,51	73,88	76,75	71,16	74,98
Thou SW	31,94	30,13	32,46	29,91	34,89	33,88	37,73	34,92	31,99	31,26	33,98	28	32,03	27,91	32,35	34,82	26,39	26,97	24,98	31,61	36,75	36,08	24,49	21,67
Mean	33,8	32,11	33,6	32,36	34,95	35,24	36,47	33,62	33,18	32,07	34,23	31,51	32,98	32,86	34,66	34,49	30,36	29,72	29,71	33,31	34,31	34,95	29,87	30,04
	Müfitbey	Atay-85	Cetinel-2000	Bayraktar-2000	Alpu-01	Bezostaja-1	Rumeli	Tosunbey	ES 26	Reis	Palandöken-97	Ayyıldız	Altay-2000	Yıldırım	Eser	Demir-2000	Gerek-79	Yunus	Sultan-95	Sönmez-2001	Atay-85	Zencirci	İkizce	Harmankaya-99
Mean	76,94	71,16	71,38	76,19	73,68	78,54	80,49	75,94	73,9	71,37	79,65	71,67	70,3	73,75	73,63	76,29	71,81	66,97	73,21	73,9	72,54	72,81	69,23	73,27
Chlorop b	29,41	29,54	27,61	31,29	33,44	32,39	31,68	31,27	31,16	30,82	29,99	29,88	29,79	28,91	28,59	28,75	28,96	28,06	28,04	27,98	27,91	27,96	27,94	27,93
Chlorop a	15,06	14,51	15,77	13,93	18,87	17,94	17,12	16,91	16,48	16,15	15,43	15,39	14,99	14,02	14,01	13,99	13,84	13,82	13,39	13,25	13,21	13,13	13,26	13,16
SPAD	54,04	44,92	47,31	51,31	59,59	59,87	57,29	56,06	55,44	54,11	51,79	51,02	50,03	47,48	46,72	46,09	46,98	45,59	45,71	44,41	43,89	43,79	43,81	43,83
Spike L	8,92	7,94	8,28	8,21	9,84	9,41	8,38	8,52	8,26	8,28	8,54	7,95	8,26	8,57	8,61	7,94	8,89	8,91	8,15	8,09	8,16	8,06	7,92	7,73
Seed W/Sp	1,35	1,30	1,32	1,34	1,44	1,43	1,42	1,41	1,42	1,42	1,42	1,39	1,38	1,39	1,37	1,34	1,34	1,34	1,28	1,11	1,10	1,09	1,06	1,00
Spike N/m2	310,23	282,02	289,38	301,03	268,13	329,01	350,07	304,12	296,11	282,11	341,14	272,01	260,14	298,24	284,11	331,97	290,11	265,07	289,00	293,89	298,01	294,79	267,81	317,93
SeedN/Sp	36,21	33,34	33,43	36,38	42,49	41,00	37,02	35,54	31,2	28,27	32,45	43,89	42,03	37,98	35,99	30,91	29,17	36,03	40,91	36,95	34,69	31,69	27,78	25,94
Plant H	90,02	86,59	76,89	99,72	89,96	84,58	88,54	89,41	84,41	85,28	98,06	82,34	85,29	91,58	99,21	85,38	87,77	82,19	88,64	97,57	84,41	87,95	90,45	86,47
Heading D	218,77	206,54	209,21	213,21	206,24	203,65	207,68	210,34	208,87	201,97	212,45	207,65	206,36	204,65	212,65	211,68	206,46	213,57	211,87	210,98	209,34	214,87	207,78	204,44
Seed Y	5,36	4,94	4,57	5,47	6,84	6,07	5,68	5,79	5,62	5,26	5,27	5,19	4,74	4,66	5,07	4,81	4,59	5,13	5,11	4,81	4,68	4,77	4,51	4,26

Table 2. Evaluation of the yield and qualiy components examined by the conditional formatting method.

Çetinel-2000 genotype had the highest value in micro sedimentation. Rumeli, Palandöken-97, Eser, Demir-2000 and Zencirci genotypes were the best ones in quality components (Table 2). As a result, when the yield and quality componentss are considered together, Bezostaja-1, Rumeli and Palandöken-97 genotypes gave higher performance in yield and quality varieties.

Principal Component Analysis

Principal component analysis is so useful method in terms of defining, classifying and evaluating the examined components. In other words, considering the correlation ratios between the components, the variations among them are evaluated and fewer important variables are determined [40, 41]. The evaluations made according to the principal component and biplot analyses in our study were given in Table 3. As seen from Table 3, the variances of the other components were evaluated based on seed yield and protein.

Plant height, seed number and weight, SPAD, chlorophyll a and b were revealed as interacting analyses with yield. Micro sedimentation, thousand seed weight and test weight were also important quality components interacting with protein content. If the biplot analysis is examined, the components affecting the yield formed one group, while the other components affecting the quality formed another group. The heading date constituted the separate group. Along with seed yield, seed number and weight, SPAD, chlorophyll a and b, spike length were important components affecting yield. Similarly, thousand seed weight, test weight, micro sedimentation and spike number/m² were revealed as components affecting the quality. Considering all the examined components, Bezostaja-1, Alpu-01, Rumeli, Palandöken-97, Tosunbey, Es-26, Müfitbey cultivars were expressed as high yield and quality genotypes.

analysis.							
	PC1	PC ₂	PC ₃	Variable	PC1	PC ₂	PC ₃
Eigenvalue	6,1980	2,4096	1,8121	Seed W/Sp	0,310	0,197	-0,105
Proportion	0,443	0,172	0,129	Spike L	0,265	0,237	0,115
Cumulative	0,443	0,615	0,744	Thou SW	0,073	-0,123	0,420
Variable	PC ₁	PC ₂	PC ₃	Test W	0,109	-0,301	0,110
Seed Y	0,343	0,253	0,150	Protein C	0,246	-0,430	-0,231
Heading D	-0,076	0,003	0,533	Micro Sed	0,155	-0,429	-0,149
Plant H	0,016	-0,023	0,630	SPAD	0,367	0,161	0,009
Seed N/Sp	0,199	0,201	0,014	Chlorop A	0,367	0,107	-0,175
Spike N/m ²	0,135	-0,380	0,205	Chlorop B	0,348	0,103	0,040

Table 3. Evaluations on yield and quality components according to principal component and biplot



Factor Analysis

In this study, factor analysis is another form of analysis. Although factor analysis is similar to principle component analysis, it shows relative differences in practice. In this analysis, the number of variables is reduced by gathering the related components under a group, and the characteristics of the components examined with these few components are analysed. By rotating the obtained results, more efficient and less number of factors is obtained, and thus clearer results are revealed. In other words, the correlation importance and priorities of the examined components are gathered together and explained as factors [42, 43]. The factor analysis performed in our study was given in Table 4.

			K	MO and B	artlett's Test	t			
Kaiser-Mey	er-Olkin M	easure of S	ampling Adeq	uacy					0,629
				Approx. C	hi-Square				381,430
Bartlett's T	est of Spher	icity		df	-				91
	-			Sig.					0,000
			Te	otal Varian	ce Explained	1			
				Extract	ion Sums of	Squared	Rotatio	on Sums of S	guared
	Init	ial Eigenva	lues		Loadings	•		Loadings	•
Component	Total	Variance %	Cumulative %	Total	Variance %	Cumulative %	Total	Variance %	Cumulative %
1	6,193	44,234	44,234	6,193	44,234	44,234	5,078	36,274	36,274
2	2,413	17,237	61,472	2,413	17,237	61,472	3,329	23,781	60,054
3	1,812	12,942	74,414	1,812	12,942	74,414	1,778	12,702	72,756
4	1,116	7,973	82,387	1,116	7,973	82,387	1,348	9,631	82,387
]	Rotated Com	ponent Matrix	ĸ			
	Factor	Factor	2 Factor ₃	Factor ₄		Factor ₁	Factor ₂	Factor ₃	Factor ₄
Seed Y	0,93	3 0,12	0,184	-0,083	Thou SW	0,290	0,81.	3 0,103	0,034
Heading D	-0,20	1 -0,04	1 0,79 6	-0,267	Test W	0,339	0,602	2 0,464	0,376
Plant H	0,08	6 -0,09	00 0,801	0,278	Protein C	0,132	0,942	2 -0,220	0,041
SeedNS/p	0,46	9 0,20	0,137	-0,610	Micro See	d 0,147	0,964	4 -0,098	-
									0,003
SpikeNM2	0,10	1 0,44	43 0,189	0,725	SPAD	0,932	0,23	1 -,030	0,084
SeedW/Sp	0,81	2 0,15	-0,162	-0,064	Chlorop A	A 0,862	0,35	1 -0,250	-
	00				~				0,003
Spike L	0,69	8 0,13	38 0,203	-0,349	Chlorop l	B 0,966	0,084	4 -0,016	0,132

Table 4. Factor analysis, made in yield and quality components.

In the analysis, the Kaiser-Meyer-Olkin proficiency measure was found to be above 0.5, and the Barlett test was determined as very important. The analyses were concluded in 3 stages, and as a result of the analysis, the important components affecting the seed yield were determined as chlorophyll a and b, SPAD, seed number and weight/spike. Again, the components affecting the protein were determined as micro sedimentation, thousand seed weight and plant height.

Correlation and Path Analyses

Correlation, varying between +1 and -1 values, shows the strength of the relationship between two or more component. Positive values indicate a positive relationship between components, and negative relationships indicate a negative relationship between components. Correlation analysis shows the strength of the relationship between components, examined in many scientific studies, including agricultural studies [43, 44, 45]. Path analysis is also an analysis based on the grading of significance depending on the correlation coefficient power of the independent components on the dependent variable [45, 46]. In this analysis, the effect of the correlation coefficients is taken into consideration and the effect of the independent components on the dependent variable is determined by ordering them from the most important to the least important. The correlation coefficients between the components examined in our study and the path

analysis showing the effect of other components on seed yield and protein content, considered as dependent components, were given in Table 5.

Table 5. The correlation coefficients and path analysis between components with the seed yield and protein content(dependent variables).

	Seed Y	Heading D	Plant H	Seed N/Sp	Spike N/m ²
Heading D	0,008 ns				
Plant H	0,152 ns	0,345 ns			
Seed N/Sp	0,521**	-0,004 ns	0,030 ns		
Spike N/m ²	0,113 ns	0,001 ns	0,185 ns	-0,200 ns	
Seed W/Sp	0,667**	-0,308 ns	-0,019 n s	0,465 ns	0,103 ns
Spike L	0,687**	0,141 ns	0,076 ns	0,421*	-0,010 ns
Thou SW	0,445*	0,019 ns	0,033 ns	0,219 ns	0,376 ns
Test W	0,422 ns	0,085 ns	0,461*	0,212 ns	0,596**
Protein C	0,189 ns	-0,310 ns	-0,159 ns	0,185 ns	0,376 ns
Micro Sed	0,215 ns	-0,127 ns	-0,137 ns	0,214 ns	0,415*
SPAD	0,885**	-0,150 ns	-0,014 ns	0,389 ns	0,268 ns
Chlorop A	0,817**	-0,322 ns	-0,188 ns	0,370 ns	0,169 ns
Chlorop B	0,931**	-0,254 ns	0,100 ns	0,381 ns	0,180 ns
	Seed W/Sp	Spike L	Thou SW	Test W	Protein C
Spike L	0,564**				
Thou SW	0,376 ns	0,230 ns			
Test W	0,255 ns	0,232 ns	0,572**		
Protein C	0,285 ns	0,202 ns	0,745**	0,522**	
Micro Sed	0,292 ns	0,256 ns	0,751**	0,576**	0,968**
SPAD	0,754**	0,622**	0,446*	0,459*	0,325 ns
Chlorop A	0,714**	0,608**	0,483*	0,376 ns	0,507*
	0,727**	0,592**	0,399*	0,429*	0,217 ns
	Micro Sed	SPAD	Chlorop A		
SPAD	0,385 ns				
Chlorop A	0,514*	0,930**			
	0,208 ns	0,933**	0,873**		



As seen in the table, seed yield and seed number and weight/spike, spike length, thousand seed weight, SPAD, chlorophyll a and b were found to be positively and

significantly related components. The protein content and thousand seed weight, test weight, micro sedimentation, SPAD were positively and significantly correlated. In Path analysis, the seed number and weight/spike, chlorophyll a and b, SPAD were found as effective components in seed yield. Micro sedimentation, thousand seed weight, test weight and seed yield were the components affecting protein content. Again, Bezostaja-1, Palandöken-97, Tosunbey, ES-26, Rumeli, Müfitbey varieties were determined as high performance and stable genotypes for yield and quality components. Multiple Linear Stepwise Regression Analysis

Multiple linear stepwise regression analysis, a sub-analysis of regression analysis, is a safe method widely used in scientific studies. The components discussed in this analysis are categorized and grouped as dependent and independent components. Therefore, this analysis reveals the important form of the relationship between the dependent variable and the independent components [47, 48]. In the multiple linear stepwise regression analysis, the effects of the independent components on the dependent component are handled according to the degree of importance [49]. Seed yield and protein content were analysed separately in the multiple linear stepwise regression analysis performed in our study. In the multiple linear stepwise regression analysis examined in the three-step model, the effect of the other examined independent regressions on the seed yield, which was considered as the dependent component, was found to be significant at the level of 1% (R2: 94.7%). Again, chlorophyll b, heading date and seed number/spike seed yield components had significant effect on seed yield. Again, the effect of the independent components on the protein content was concluded in five model steps and these effects were significant at the 1% level. (R2: 99.4%). Micro sedimentation, heading date, SPAD, chlorophyll a and b had a significant effect on protein content.

Seed Vield				Model Su	nmary		
Model		R	\mathbb{R}^2	intouch bui	Adjusted R ²	Estimate S _x	
1			0,931	0,867	0,861		0,225
2			0,965	0,931	0,924		0,167
3			0,977	0,954	0,947		0,139
Protein Co	ntent			Model Sum	mary		
Model		R	\mathbb{R}^2		Adjusted R ²	Estimate S _x	
1			0,968	0,936	0,933		0,237
2			0,986	0,971	0,969		0,162
5			0,998	0,996	0,994		0,070
Seed Yield ^a	I			ANOVA			
Model			Sum of Squares	df	Mean Square	F S	ig.
1	Regression		7,310	1	7,310	143,713	0,000 ^b
	Residual		1,119	22	,051		
	Total		8,429	23			
2	Regression		7,845	2	3,922	140,851	0,000°
	Residual		0,585	21	0,028		
	Total		8,429	23			
3	Regression		8,042	3	2,681	138,236	0,000 ^d
	Residual		0,388	20	0,019		
	Total		8,429	23			

Table 6. Multiple linear stepwise regression analysis showing the effect of independent variables on seed yield and protein content (dependent variables).

a. Dependent Variable: SeedY b. Predictors: (Constant), Chlorop B c. Predictors: (Constant), Chlorop B, Heading D d. Predictors: (Constant), Chlorop B, Heading D, Seed N/Sp

Protein Content ^a		ANOVA								
Model		Sum of Squares	df	Mean Square	F	Sig.				
1	Regression	18,166	1	18,166	322,520	0,000 ^b				
	Residual	1,239	22	0,056						
	Total	19,406	23							
2	Regression	18,851	2	9,426	356,988	0,000 ^c				
	Residual	0,554	21	0,026						
	Total	19,406	23							
5	Regression	19,319	5	3,864	800,668	0,000 ^f				
	Residual	0,087	18	0,005						
	Total	19,406	23							
a Dane	andant Vaniables Destain(h Duadiatana (Constant) Mises	ad a Duadiatana	(Constant) Miona Cad Has	ding D f Duadiata	(Constant)				

Dependent Variable: ProteinC b. Predictors: (Constant), MicroSed c. Predictors: (Constant), Micro Sed, Heading D f. Predictors: (Constant), Micro Sed, Heading D, SPAD, Chlorop B, Chlorop A Seed Yield Coefficients

				Standardized		
		Unstandardized Co	oefficients	Coefficients		
Model		В	Sx	Beta	t	Sig.
1	(Constant)	-4,745	0,825		-5,753	0,000
	Chlorop B	0,337	0,028	0,931	11,988	0,000
2	(Constant)	-17,687	3,017		-5,862	0,000
	Chlorop B	0,361	0,022	0,997	16,784	0,000
	HeadingD	0,059	0,013	0,260	4,380	0,000
3	(Constant)	-16,913	2,529		-6,687	0,000
	Chlorop B	0,337	0,020	0,930	17,239	0,000
	Heading D	0,055	0,011	0,244	4,888	0,000
	Seed N/Sp	0,021	0,007	0,166	3,187	0,005
Protein Content			Coef	ficients		
				Standardized		
		Unstandardized Co	oefficients	Coefficients		
Model		В	Sx	Beta	t	Sig.
	(Constant)	-3,049	0,795		-3,836	0,001
	Micro Sed	0,984	,055	0,968	17,959	0,000
2	(Constant)	10,815	2,776		3,895	0,001
	Micro Sed	0,960	00,038	0,944	25,376	0,000
	Heading D	-0,065	0,013	-0,189	-5,092	0,000
5	(Constant)	1,502	1,679		0,894	0,383
	Micro Sed	1,044	0,023	1,027	45,154	0,000
	Heading D	0-,039	0,007	-0,115	-5,822	0,000
	SPAD	-0,109	0,012	-0,632	-9,093	0,000
	Chlorop B	0,233	0,030	0,425	7,814	0,000
	Chlorop A	0,088	0,032	0,158	2,765	0,013

Desicion Tree Analysis

The decision tree graphs dealing with seed yield and quality components were shown in Figures 1 and 2. In the decision tree graph (Figure 1), where the seed yield is discussed, the main shaping factor for the seed yield was determined as SPAD.



SPAD Main Determinant						
If SPAD ≤43,490 SY is 4,345 Heading D Main Determinant	If SPAD 49,870-53,950 SY is 5,356 Heading D Main Determinant					
If Heading $D \le SY$ is 4,290 If Heading $D > SY$ is 4,400	If Heading D≤ 207,370 SY is 5,240 If Heading D 204,370-					
If SPAD 43,490-49,870 SY is 4,789 Spike N/m ² Main Determinant	205,960 SY is 5,230					
If Spike N/m ² ≤ 286,310 SY is 5,000 Plant H Main Determinant	If Heading D 20,960-208,140 SY is 5,200 If Heading D					
If Plant H ≤ 82,190 SY is 5,070, If Plant H 82,190-85,380 SY is	208,140-210,530 SY is 5,5770					
4,870, If Plant H 85,38087,770 SY is 4,900	If Heading D > 210,530 SY is 5,340					
If Plant H 87,770-89,960 SY is 5,060, If Plant H> 89,960 SY is	If SPAD 53,950-57,160 SY is 5,737 Heading D Main Determinant					
5,100	If Heading D ≤ 205,770 SY is 5,590 If Heading D 205,770-					
If Spike N/m ² > 286,310 SY is 4,689 Chlorop B Main Determinant	205,960 SY is 5,750					
If Chlorop B ≤ 27,530 SY is 4,470, If Chlorop B 27,530-28,250	If Heading D \leq 205,960 SY is 5,870					
SY is 4,702, If Chlorop B > 28,250 SY is 4,595	If SPAD > 57,160 SY is 6,445 Heading D Main Determinant					
-	If Heading D ≤ 205,310 SY is 6,100 If Heading D > 205,310					
	SY is 6,790					

Figure 1. Decision tree graph of the components affecting seed yield.

Under the SPAD, heading date and spike number/m2 were determined as secondary important components. After that, plant height and chlorophyll b emerged as important components. In the decision tree graph, the seed yield varied about 4.2 t/ha and 5.9 t/ha. This means that the seed yield significantly increased when optimum yield component values were obtained. In the studies carried out, spike number/m2, chlorophyll related components (SPAD, chlorophyll a and b), heading date and plant height were found as important yield components, and they have both direct and indirect effects on the seed yield [50, 51]. It has also been mentioned that spike number/m2 and chlorophyll b had important effect in seed yield [52].

When the quality of wheat is considered, the first components that come to mind are protein content and sedimentation amount. The high levels of these components, together with the high yield, make wheat varieties stand out as preferred varieties. Today, in breeding studies, varieties with high protein content and sedimentation as well as high yield are preferred and traded [53, 54]. Wheat varieties with protein higher than 12% in wheat gain importance as bread wheat, but those with less than 11% are preferred as biscuit wheat [55, 56]. In recent years, as a result of the development of the biscuit industry and the increase in the demand for biscuits in the societies, the consumption of biscuits has increased rapidly. As a result, the trade of low protein and sedimentation genotypes has also increased rapidly [57, 58]. The decision tree graph of the components affecting the protein content was given in Figure 2.

In our study, the most influential component on the protein content was naturally determined as micro sedimentation. According to many studies, high sedimentation amount indicates high protein and low protein content leads to a feature to be evaluated in the biscuit industry with low protein content [53, 54]. In our study, although microsedimentation, which emerged as the main determinant, was low, the main determinant was seed yield and thousand-seed weight, but with the increase of micro-sedimentation, seed yield and the number of days to spike were more effective. From this, it becomes clear that micro-sedimentation is closely related to yield and is also shaped by the thousand-seed weight and the number of days to spike. Micro sedimentation showed a variation of about 9.8 to 12.9 ml. As a result, micro-sedimentation increased with the increase in seed yield and thousand seed weight, and thus, an increase in protein occurred. As a result of both tree plots, seed yield and protein content are affected by environmental conditions, but they can also vary depending on plant performance, that is, genetic capacity. The increase in this genetic capacity increases depending on the high photosynthetic capacity and the increase in agronomic characteristics, and this situation affects the quality and yield considerably.





Phyton Regression Analysis

Phyton regression analysis, which is a statistical method, is used to examine the effects of dependent and independent variables on each other and to express them with a mathematical model [59]. There are different regression models to examine the relationship between variables [60]. A cause-effect relationship is sought between the variables and an interpretation can be made on the relationship. In this mathematical model, if the number of independent variables is one, it is called a simple regression model, and if it is more than one, it is called a multiple regression model. The main purpose here is to create an estimation equation that enables analysis of dependent variables using independent variables [61]. In this study, multiple regression analysis was performed using multiple independent variables, while seed yield was the dependent variable. In this analysis, the equation to be used is as follows: γ the seed yield value as the dependent variable, the independent variables X1,X2 ... Xn and β 0, β 1, β 2.... Bn represents the parameters of the independent variables. In addition, β 0 represents the constant term and ε the error term.

$$\gamma = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_n X_n + \varepsilon$$
 Formula 1

The Anaconda distribution system was used to construct and use the multiple regression model. To build and analyse the model, the "Jupyter Notebook" interface in Anaconda and python version 3.8.8 were used. The sklearn library was used to create the model, and the matplotlib library was used to visualize the values. At the end of the model training, the coefficients of the variables were obtained and the analysis was performed.

After the multiple regression model, the coefficient values showing the effect of the independent variables on the dependent variable, the seed yield, were given in Table.

	Variables	Coefficient	Absolute Coefficient
X11	Chlorophyll b	0,395176	0,395176
X10	Chlorophyll a	0,122830	0,122830
X1	Heading Date	0,072892	0,072892
X9	SPAD	-0,053253	0,053253
X5	Seed Weight/Spike	-0,028668	0,028668
X6	Spike Length	0,026521	0,026521
X3	Seed Number/Spike	0,022607	0,022607
X_8	Test Weight	-0,017992	0,017992
X_7	Thousand Seed Weight	0,005082	0,005082
X4	Spike Number/m ²	0,001500	0,001500
\mathbf{X}_2	Plant Height	0.000861	0.000861

Table 7. Coefficient values showing the effect of independent variables on thedependent variable, seed yield.



The values of the coefficient of influence of the independent variables on the dependent variable, the seed yield, are given in order from largest to smallest. As a result of the analysis made here, chlorophyll b, chlorophyll a and heading date values, whose values are given exactly, have a positive coefficient. On this seed yield, chlorophyll b has a high positive effect, and chlorophyll a and heading date have a moderate positive effect. After the multiple regression model, the coefficient values showing the effect of the independent variables on the dependent variable, the protein content, were given in Table 8.

Table 8. Coefficient values showing the effect of independent variables on the dependent variable, protein content.

	Variables	Coefficient	Absolute Coefficient
X10	Micro Sedimentation	1,001712	1,001712
X13	Chlorophyll b	0,150881	0,150881
\mathbf{X}_{1}	Seed Yield	0,123443	0,123443
X11	SPAD	-0,099671	0,099671



It has been revealed that the component affecting the protein content, the dependent variable, were micro sedimentation, chlorophyll b and seed yield. As a result of both analyses, chlorophyll a and b, heading date and micro sedimentation components were found as the most effective components on seed yield and quality. As a result of the analyses made, the components affecting seed yield and protein content, and the genotypes determined to be superior performance were given in Table 9.

Table 9.	The components affecting seed yield an	id protein content, and the genotypes
	determined to be superior	performance.

	Conditional Formatting	Principal Component	Biplot	Factor	Correlation	Path	Stepwise Regression	Decision Tree	Pyhton Regreeion
Yield									
ling Date	۲								
Height									
Number/Spike			۲						
e Number/m ²									
Weight/Spike			۲						
e Length			۲						
sand Seed	۲		۲						
ht									
Weight	۲		۲						
ein Content									
0	۲		۲			۲			۲
nentation									
D	۲		۲			۲		۲	
rophyll A									۲
rophyll B				۲					۲
D rophyll A rophyll B stypes	● ● Bezostaja-1, R	♥ ♥ Rumeli ve Paland	♥ ♥ ● öken-97, A	9 9 1pu-01, Tos	• • • • • •	e e üfitbey		9 9 9	8 8 8 8

In the light of Table 9, seed number/spike, seed weight/spike, micro sedimentation, SPAD, chlorophyll a and chlorophyll b were effective components on seed yield and protein content. More detailed studies are needed on this subject. More successful results can be obtained in breeding studies with detailed analyses to be made.

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